

SEQUENCE LISTING

<110> Larsen, Christian P.
Pearson, Thomas C.
Waller, Edmund K.
Adams, Andrew B.

<120> METHODS OF INDUCING ORGAN TRANSPLANT TOLERANCE AND
CORRECTING HEMOGLOBINOPATHIES

<130> D0136NP/30436.58USU1

<140> Not yet known
<141> 2002-01-25

<150> 60/264,528
<151> 2001-01-26

<150> 60/303,142
<151> 2001-07-05

<160> 20

<170> PatentIn Ver. 2.1

<210> 1
<211> 1152
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EIg
sequence

<400> 1
atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
acagtgtctt ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggg acgtggacgg cgtggaggtg 660
cataatgcc aagacaaagcc gcgaggagg cagtacaaca gcacgtaccg tgtgggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

<210> 2
 <211> 383
 <212> PRT
 <213> Artificial Sequence

5

<220>
 <223> Description of Artificial Sequence: L104E1g
 sequence

10

<400> 2
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15

15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

20

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

25

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

30

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

35

Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160

40

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175

45

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205

50

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

55

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 245 250 255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

5 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

10 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

20 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

25
<210> 3
<211> 1152
<212> DNA

30 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: L104EA29YIg
sequence

35
40
45
50
55
<400> 3
atgggtgtac tgctcacaca gaggacgctg ctacagtctgg tccttgcaact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtagtggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
acagtgtctt ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataaggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg 660
cataatgcc aagacaaagcc gggggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720
gtcctcaccg tctgcacca ggactggctg aatggcaagg agtacaagtg caagggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
tgctcogtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

<210> 4
 <211> 383
 <212> PRT
 5 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: L104EA29YIg
 sequence

10 <400> 4
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 15 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 20 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125
 35 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160
 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175
 45 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205
 50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys

245

250

255

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

5

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

10

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

15

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

20

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

25

<210> 5

<211> 1152

30

<212> DNA

<213> Artificial Sequence

<220>

35

<223> Description of Artificial Sequence: L104EA29LIg
sequence

<400> 5

40

atgggtgtac tgctcacaca gaggacgctg ctcagtcttg tccttgcaact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactaggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aattgactga ggtccgggtg 180
acagtgtctt ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcc agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataaggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggtg 600
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg 660
cataatgcc aagacaaagcc gcgaggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caagggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccagggtcagc 900
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cgggtccttc 1020
55 ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

5 <210> 6
 <211> 383
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence: L104EA29LIg
 sequence

15 <400> 6
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Leu Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125
 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160
 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175
 45 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205
 50 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

15 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

<210> 7

30 <211> 1152

<212> DNA

<213> Artificial Sequence

<220>

35 <223> Description of Artificial Sequence: L104EA29TIg
sequence

<400> 7

40 atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aaactactga ggtccgggtg 180
acagtgcttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
45 gagctcatgt acccaccgcc atactacgag ggcataggca acggaacca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctgggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtgggtggg 600
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg 660
50 cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtgggtcagc 720
gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
55 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctcctgtct 1140

5 <210> 8
 <211> 383
 <212> PRT
 <213> Artificial Sequence

10 <220>
 <223> Description of Artificial Sequence: L104EA29TIg
 sequence

15 <400> 8
 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
 1 5 10 15
 Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30
 20 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45
 Tyr Ala Ser Pro Gly Lys Thr Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60
 25 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80
 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95
 30 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110
 35 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125
 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140
 40 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
 145 150 155 160
 45 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 165 170 175
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 180 185 190
 50 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 195 200 205
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 210 215 220
 55 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

5 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

10 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

15 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

20 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

25 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

30 <210> 9
<211> 1152
<212> DNA
<213> Artificial Sequence

35 <220>
<223> Description of Artificial Sequence: L104EA29WIg
sequence

<400> 9

40 atgggtgtac tgctcacaca gaggacgctg ctcagtctgg tccttgcaact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggactggc cagcagccga 120
ggcatcgcta gctttgtgtg tgagtatgca tctccaggca aatggactga ggtccgggtg 180
acagtgtctc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttctt agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
45 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacgag ggcataaggca acggaaccca gatttatgta 420
attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
ccaaaaccca aggacacctt catgatctcc cggacccttg aggtcacatg cgtgggtggtg 600
50 gacgtgagcc acgaagacc tgagggtcaag ttcaactggg acgtggacgg cgtggaggtg 660
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
gtcctcaccg tcttgacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
aacaagccg tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
gaaccacagg tgtacacctt gccccatcc cgggatgagc tgaccaagaa ccaggctcagc 900
55 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
gggcagccgg agaacaacta caagaccag cctcccgtgc tggactccga cggctccttc 1020
ttcctctaca gcaagctcac cgtggacaag agcagggtggc agcaggggaa cgtcttctca 1080

tgtctcgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
ccgggtaaat ga 1152

5 <210> 10
<211> 383
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence: L104EA29Wlg
sequence

<400> 10

15 Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

20 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

25 Tyr Ala Ser Pro Gly Lys Trp Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

30 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

35 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

40 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

45 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
165 170 175

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
180 185 190

50 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
195 200 205

55 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
210 215 220

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser

225 230 235 240

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
245 250 255

5

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
260 265 270

10

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
275 280 285

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
290 295 300

15

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
305 310 315 320

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
325 330 335

20

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
340 345 350

25

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
355 360 365

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375 380

30

<210> 11
<211> 636
<212> DNA
<213> Homo sapiens

35

<400> 11
atgggtgtac tgctcacaca gaggacgctg ctcaagtctgg tccttgcaact cctgtttcca 60
agcatggcga gcatggcaat gcacgtggcc cagcctgctg tggtagctggc cagcagccga 120
ggcatcgcca gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
40 acagtgcctt ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
gggaatgagt tgaccttccct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
gagctcatgt acccaccgcc atactacctg ggcataggca acggaacca gatttatgta 420
attgatccag aaccgtgccc agattctgac ttctctctct ggatccttgc agcagttagt 480
45 tcgggggttg ttttttatag ctttctctct acagctgttt ctttgagcaa aatgctaaag 540
aaaagaagcc ctcttacaac aggggtctat gtgaaaatgc cccaacaga gccagaatgt 600
gaaaagcaat ttcagcctta ttttattccc atcaat 636

50

<210> 12
<211> 212
<212> PRT
<213> Homo sapiens

55

<400> 12
Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
 20 25 30

5 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
 35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
 50 55 60

10 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
 65 70 75 80

15 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
 85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
 100 105 110

20 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
 115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
 130 135 140

25 Pro Cys Pro Asp Ser Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser
 145 150 155 160

30 Ser Gly Leu Phe Phe Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser
 165 170 175

Lys Met Leu Lys Lys Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys
 180 185 190

35 Met Pro Pro Thr Glu Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe
 195 200 205

Ile Pro Ile Asn
 210

40

<210> 13

<211> 1152

<212> DNA

45 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CTLA4Ig
 sequence

50

<400> 13

atgggtgtac tgctcacaca gaggacgctg ctacgtctgg tccttgcaact cctgtttcca 60
 agcatggcga gcatggcaat gcacgtggcc cagctgctg tggactggc cagcagccga 120
 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
 55 acagtgttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360

gagctcatgt acccaccgcc atactacctg ggcataaggca acggaaccca gatttatgta 420
 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
 acatccccac cgtccccagc acctgaactc ctgggtggat cgtcagtctt cctcttcccc 540
 5 ccaaaaccca aggacaccct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
 gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggtggtg 660
 cataatgccca agacaaagcc gcgaggaggag cagtacaaca gcacgtaccg ggtggtcagc 720
 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctcc 780
 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
 10 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
 ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
 gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggctccttc 1020
 ttctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca 1080
 tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct 1140
 15 ccgggtaaat ga 1152

<210> 14

<211> 383

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CTLA4Ig
sequence

<400> 14

Met Gly Val Leu Leu Thr Gln Arg Thr Leu Leu Ser Leu Val Leu Ala
1 5 10 15

Leu Leu Phe Pro Ser Met Ala Ser Met Ala Met His Val Ala Gln Pro
20 25 30

Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
35 40 45

Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
50 55 60

Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
65 70 75 80

Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
85 90 95

Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
100 105 110

Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
115 120 125

Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
130 135 140

Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
145 150 155 160

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val

	165	170	175
	Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr		
	180	185	190
5	Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu		
	195	200	205
10	Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys		
	210	215	220
	Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser		
	225	230	235
15	Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys		
	245	250	255
	Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile		
	260	265	270
20	Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro		
	275	280	285
25	Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu		
	290	295	300
	Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn		
	305	310	315
30	Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser		
	325	330	335
	Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
	340	345	350
35	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu		
	355	360	365
40	His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
	370	375	380
45	<210> 15		
	<211> 6		
	<212> PRT		
	<213> Homo sapiens		
50	<400> 15		
	Met Tyr Pro Pro Pro Tyr		
	1 5		
55	<210> 16		
	<211> 65		
	<212> DNA		
	<213> Artificial Sequence		

<220>

<223> Description of Artificial Sequence: primer
sequence encoding Oncostatin M-CTLA4 fusion

5 <400> 16
ctcagtctgg tccttgcaact cctgtttcca agcatggcga gcatggcaat gcacgtggcc 60
cagcc 65

10 <210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

15 <220>
<223> Description of Artificial Sequence: primer
sequence encoding CTLA4 sequence

20 <400> 17
tttgggctcc tgatcagaat ctgggcacgg ttg 33

25 <210> 18
<211> 72
<212> DNA
<213> Artificial Sequence

30 <220>
<223> Description of Artificial Sequence: primer
sequence encoding Oncostatin M signal peptide
sequence

35 <400> 18
ctagccactg aagcttcacc aatgggtgta ctgctcacac agaggacgct gtcagtctg 60
gtccttgcaac tc 72

40 <210> 19
<211> 41
<212> DNA
<213> Artificial Sequence

45 <220>
<223> Description of Artificial Sequence: primer
sequence from vector sequence

<400> 19
gaggtgataa agcttcacca atgggtgtac tgctcacaca g 41

50 <210> 20
<211> 42
<212> DNA
<213> Artificial Sequence

55 <220>
<223> Description of Artificial Sequence: primer

sequence encoding CTLA4 sequence

<400> 20

gtggtgtatt ggtctagatc aatcagaatc tgggcacggt tc

42

5

10057288-043502